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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/885,478

DATE: 10/04/2001

TIME: 17:56:10

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I885478.raw

ENTERED

3 <110> APPLICANT: SALON, JOHN A
 4 LAZ, THOMAS M
 5 NAGORNY, RAISA
 6 WILSON, AMY E
 8 <120> TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR
 (MCH1) AND
 9 USES THEREOF
 11 <130> FILE REFERENCE: 1795/57453-A-PCT-US
 13 <140> CURRENT APPLICATION NUMBER: 09/885,478
 C--> 14 <141> CURRENT FILING DATE: 2001-09-24
 16 <150> PRIOR APPLICATION NUMBER: PCT/US99/31169
 17 <151> PRIOR FILING DATE: 1999-12-30
 19 <160> NUMBER OF SEQ ID NOS: 28
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1269
 25 <212> TYPE: DNA
 26 <213> ORGANISM: HOMO SAPIENS
 28 <400> SEQUENCE: 1
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 31 ggctgccagg ctacggagga agaccccctt cccgactgcg gggcttgccg tccgggacaa 120
 33 ggtggcaggc gctggaggct gccgcagcct gcgtgggtgg aggggagctc agctcggttg 180
 35 tgggagcagg cgaccggcac tggttgatg gacctggaag cctcgctgct gccactggt 240
 37 cccaatgcca gcaacacctc tgatggcccc gataacctca cttcagcagg atcacctcct 300
 39 cgcacgggga gcatctccta catcaacatc atcatgcctt cggtgttcgg caccatctgc 360
 41 ctctctggga tcatcgaggaa ctccacggtc atcttcgcgg tcgtgaagaa gtccaagctg 420
 43 cactgggtgca acaacgtccc cgacatcttc atcatcaacc tctcggtagt agatctcctc 480
 45 tttctcctgg gcatgccctt catgatccac cagctcatgg gcaatggggg gtggcacttt 540
 47 ggggagacca tgtgcaccct catcacggcc atggatgcca atagtcagtt caccagcacc 600
 49 tacatcctga ccgccatggc cattgaccgc tacctggcca ctgtccaccc catctcttcc 660
 51 acgaagtccc ggaagccctc tgtggccacc ctgggtgatc gcctcctgtg ggccctctcc 720
 53 ttcacagca taccctctgt gtggctgtat gccagactca tcccttccc aggaggtgca 780
 55 gtgggctgcg gcatagcct gcccaaccca gacactgacc tctactggtt caccctgtac 840
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 59 ctgcagcgca tgacgtcctc agtggccccc gcctcccagc gcagcatccg gctgcggaca 960
 61 aagaggggtga cccgcacagc catcgccatc tgtctggtct tctttgtgtg ctgggcaccc 1020
 63 tactatgtgc tacagctgac ccagttgtcc atcagccgcc cgaccctcac ctttgtctac 1080
 65 ttatacaatg cggccatcag cttgggctat gccaacagct gcctcaaccc ctttgtgtac 1140
 67 atcgtgctct gtgagacgtt ccgcaaacgc ttggtcctgt cgggtgaagcc tgcagcccag 1200
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 75 <211> LENGTH: 422
 76 <212> TYPE: PRT
 77 <213> ORGANISM: HOMO SAPIENS
 79 <400> SEQUENCE: 2
 81 Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
 82 1 5 10 15

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85 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
86          20          25          30
89 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
90          35          40          45
93 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
94          50          55          60
97 Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
98 65          70          75          80
101 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
102          85          90          95
105 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
106          100          105          110
109 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
110          115          120          125
113 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
114          130          135          140
117 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
118 145          150          155          160
121 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
122          165          170          175
125 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
126          180          185          190
129 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
130          195          200          205
133 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
134          210          215          220
137 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
138 225          230          235          240
141 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
142          245          250          255
145 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
146          260          265          270
149 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
150          275          280          285
153 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
154          290          295          300
157 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
158 305          310          315          320
161 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
162          325          330          335
165 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
166          340          345          350
169 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
170          355          360          365
173 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
174          370          375          380
177 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
178 385          390          395          400
181 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg

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182          405          410          415
185 Thr Glu Ser Lys Gly Thr
186          420
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 1214
191 <212> TYPE: DNA
192 <213> ORGANISM: RATTUS NORVEGICUS
194 <400> SEQUENCE: 3
195 gcaggcgacc tgcaccggct gcatggatct gcaaacctcg ttgctgtcca ctggccccaa      60
197 tgccagcaac atctccgatg gccaggataa tctcacattg ccgggggtcac ctcctcgcac      120
199 agggagtgtc tctacatca acatcattat gccttccgtg tttggtacca tctgtctcct      180
201 gggcatcgtg ggaaactcca cggtcattct tgctgtggtg aagaagtcca agctacactg      240
203 gtgcagcaac gtccccgaca tcttcatcat caacctctct gtggtggatc tgctcttcct      300
205 gctgggcatg cctttcatga tccaccagct catggggaac ggcgtctggc actttgggga      360
207 aaccatgtgc accctcatca cagccatgga cgccaacagt cagttcacta gcacctacat      420
209 cctgactgcc atgaccattg accgctactt ggccaccgtc caccctatct cctccaccaa      480
211 gttccggaag cctccatgg ccaccctggt gatctgcctc ctgtgggcgc tctccttcat      540
213 cagtatcacc cctgtgtggc tctacgccag gctcattccc tcccaggagg gtgctgtggg      600
215 ctgtggcatc cgctgccaa acccggaac tgacctctac tggttcactc tgtaccagtt      660
217 tttcctggcc tttgcccttc cgtttgtggt cattaccgcc gcatacgtga aaatactaca      720
219 gcgcattgac tcttcgggtg cccagcctc ccaacgcagc atccggcttc ggacaaagag      780
221 ggtgaccgcg acggccattg ccatctgtct ggtcttcttt gtgtgctggg caccctacta      840
223 tgtgtgtcag ctgaccagc tgtccatcag ccgccgacc ctcacgtttg tctacttgta      900
225 caacgcggcc atcagcttgg gctatgctaa cagctgcctg aacccttttg tgtacatagt      960
227 gctctgtgag acctttcgaa aacgcttggg gttgtcagtg aagcctgcag cccaggggca     1020
229 gctccgcacg gtcagcaacg ctcagacagc tgatgaggag aggacagaaa gcaaaggcac     1080
231 ctgacaattc cccagtcgcc tccaagtcag gccaccccat caaacctggg ggagagatac     1140
233 tgagattaaa cccaaggcta ccctgggaga atgcagaggc tggaggctgg gggcttgtag     1200
235 caaccacatt ccac                                     1214
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 353
240 <212> TYPE: PRT
241 <213> ORGANISM: RATTUS NORVEGICUS
243 <400> SEQUENCE: 4
245 Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn
246 1          5          10          15
249 Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
250          20          25          30
253 Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
254          35          40          45
257 Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
258          50          55          60
261 Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
262 65          70          75          80
265 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
266          85          90          95
269 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
270          100         105         110
273 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe

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274          115          120          125
277 Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
278          130          135          140
281 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
282 145          150          155          160
285 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
286          165          170          175
289 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
290          180          185          190
293 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
294          195          200          205
297 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
298          210          215          220
301 Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
302 225          230          235          240
305 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
306          245          250          255
309 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
310          260          265          270
313 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
314          275          280          285
317 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
318          290          295          300
321 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
322 305          310          315          320
325 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
326          325          330          335
329 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
330          340          345          350
333 Thr

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337 <210> SEQ ID NO: 5

338 <211> LENGTH: 26

339 <212> TYPE: DNA

340 <213> ORGANISM: ARTIFICIAL SEQUENCE

342 <220> FEATURE:

343 <223> OTHER INFORMATION: PRIMER

345 <400> SEQUENCE: 5

346 gggaactcca cggatcatctt cgcggt

26

349 <210> SEQ ID NO: 6

350 <211> LENGTH: 26

351 <212> TYPE: DNA

352 <213> ORGANISM: ARTIFICIAL SEQUENCE

354 <220> FEATURE:

355 <223> OTHER INFORMATION: PRIMER

357 <400> SEQUENCE: 6

358 tagcggtcaa tggccatggc gggtcag

26

361 <210> SEQ ID NO: 7

362 <211> LENGTH: 45

363 <212> TYPE: DNA

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364 <213> ORGANISM: ARTIFICIAL SEQUENCE
366 <220> FEATURE:
367 <223> OTHER INFORMATION: PROBE
369 <400> SEQUENCE: 7
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373 <210> SEQ ID NO: 8
374 <211> LENGTH: 25
375 <212> TYPE: DNA
376 <213> ORGANISM: ARTIFICIAL SEQUENCE
378 <220> FEATURE:
379 <223> OTHER INFORMATION: PRIMER
381 <400> SEQUENCE: 8
382 cttctaggcc tgtacggaag tgttta      25
385 <210> SEQ ID NO: 9
386 <211> LENGTH: 27
387 <212> TYPE: DNA
388 <213> ORGANISM: ARTIFICIAL SEQUENCE
390 <220> FEATURE:
391 <223> OTHER INFORMATION: PRIMER
393 <400> SEQUENCE: 9
394 gttgtgggttt gtccaaactc atcaatg      27
397 <210> SEQ ID NO: 10
398 <211> LENGTH: 37
399 <212> TYPE: DNA
400 <213> ORGANISM: ARTIFICIAL SEQUENCE
402 <220> FEATURE:
403 <223> OTHER INFORMATION: PRIMER
405 <400> SEQUENCE: 10
406 cgcggatcca ttatgtctgc actccgaagg aaatttg      37
409 <210> SEQ ID NO: 11
410 <211> LENGTH: 38
411 <212> TYPE: DNA
412 <213> ORGANISM: ARTIFICIAL SEQUENCE
414 <220> FEATURE:
415 <223> OTHER INFORMATION: PRIMER
417 <400> SEQUENCE: 11
418 cgcgaattct tatgtgaagc gatcagagtt catttttc      38
421 <210> SEQ ID NO: 12
422 <211> LENGTH: 34
423 <212> TYPE: DNA
424 <213> ORGANISM: ARTIFICIAL SEQUENCE
426 <220> FEATURE:
427 <223> OTHER INFORMATION: PRIMER
429 <400> SEQUENCE: 12
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433 <210> SEQ ID NO: 13
434 <211> LENGTH: 29
435 <212> TYPE: DNA
436 <213> ORGANISM: ARTIFICIAL SEQUENCE

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/885,478

DATE: 10/04/2001

TIME: 17:56:11

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